

Figure 1

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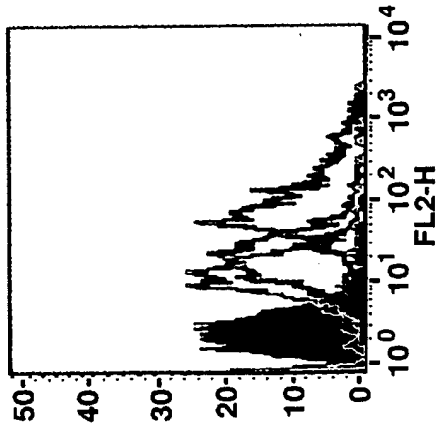
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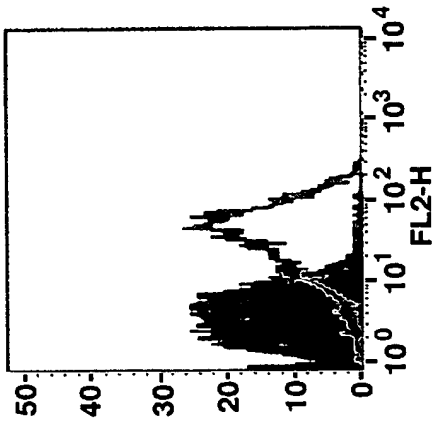
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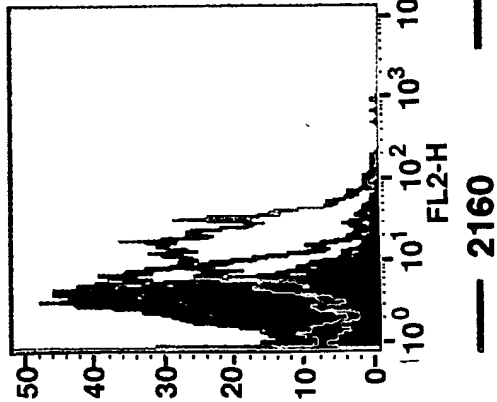
A1: BUD cells



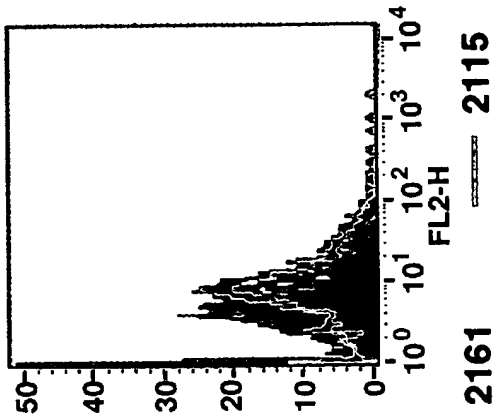
A2: TR-1 cells



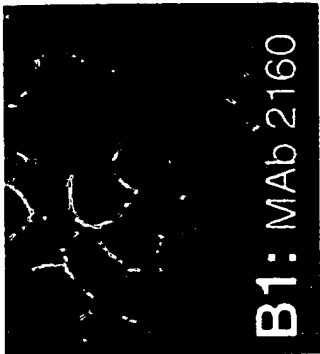
A3: RIN-F cells



A4: ASC cells



BUD cells



B1: MAb 2160

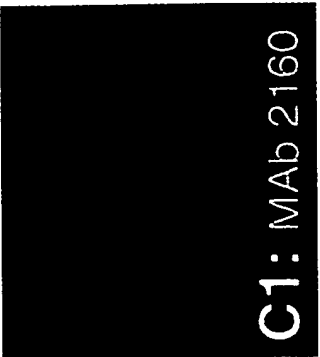


B2: MAb 2161



B3: MAb 2115

TR-1 cells



C1: MAb 2160



C2: MAb 2161



C3: MAb 2115



Figure 2

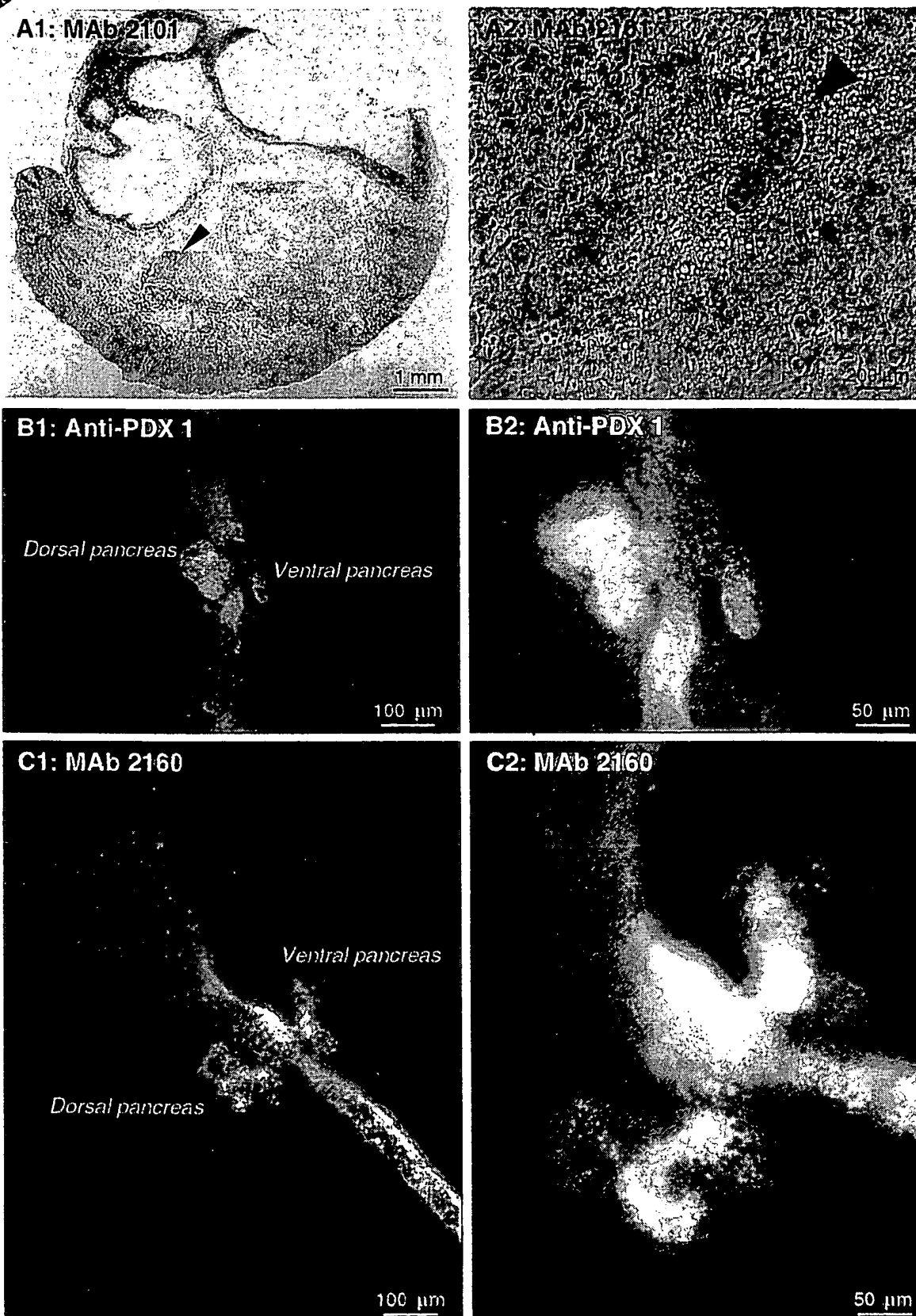
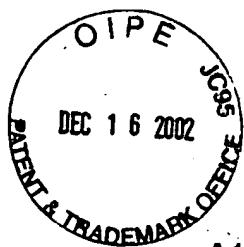


Figure 3

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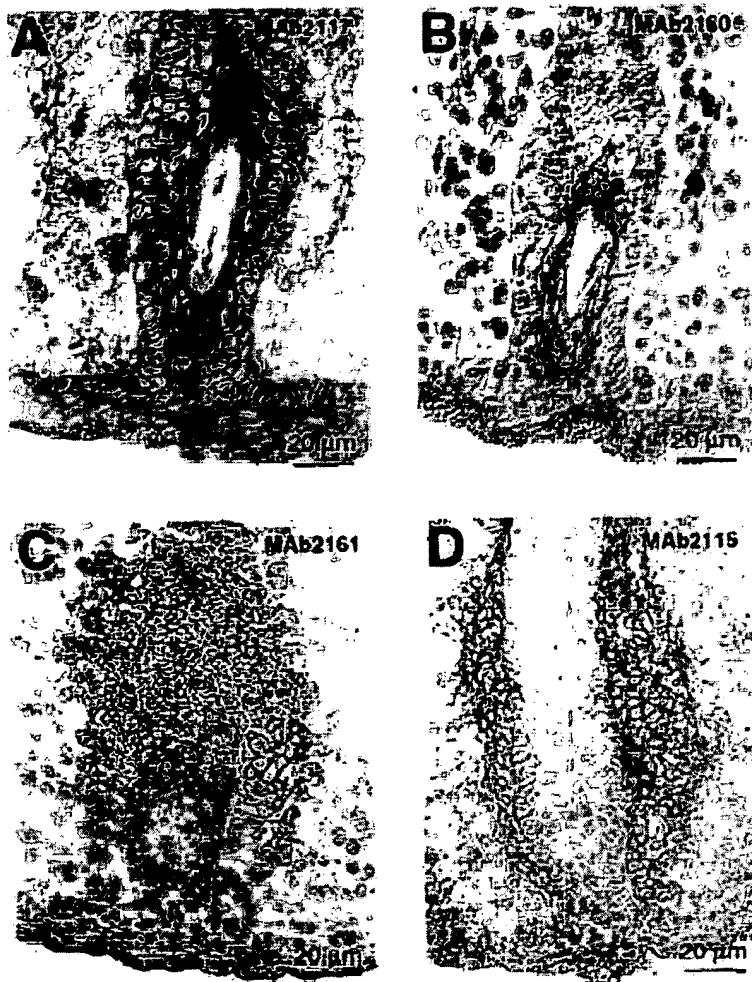


Figure 4

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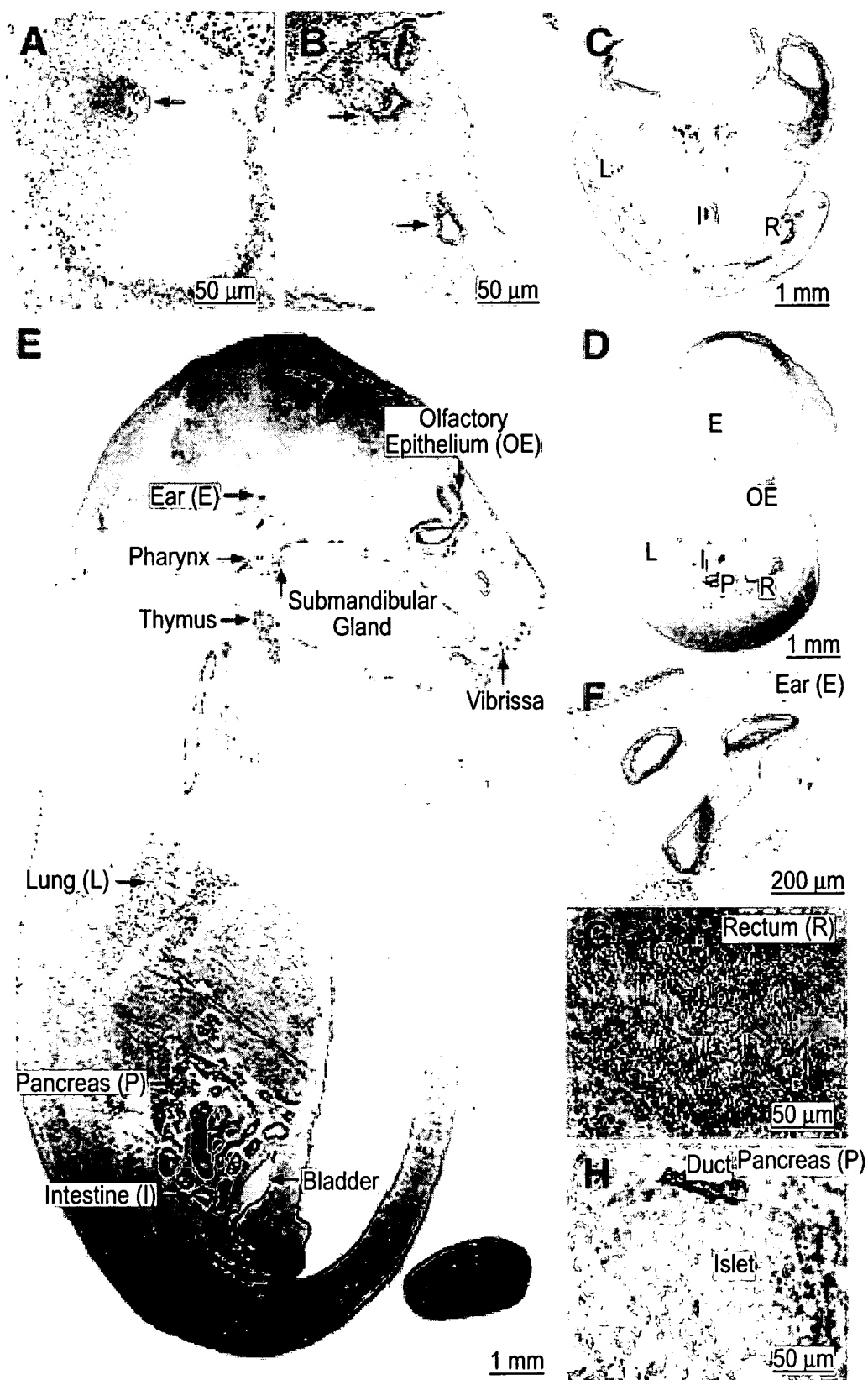


FIG. 5

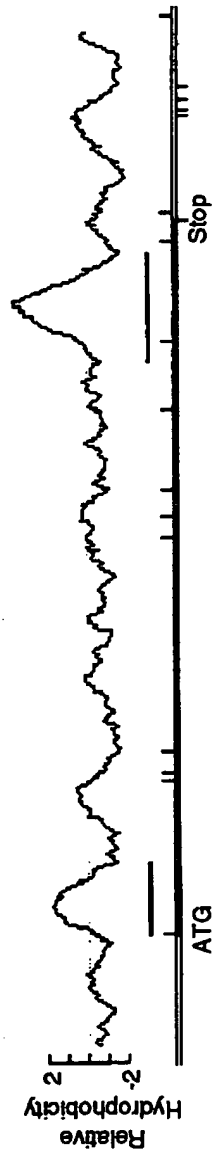


Figure 6B

B



C

Ag2160
mEGP
hEGP-2
hEGP-1

1-----MAPPKA-LAFGLLLAVVTATLAAQKDCVNNYKLT SRCYENENGECQCTSYGTQNTVICSKLASKCLVM
-----MAGPQA-LAFGLLLAVVTATLAAQKDCVNDNYKLTATSCSLNEYGECQCTSYGTQNTVICSKLASKCLAM
-----MAPPOV-LAFGLLLAAATATFAAAQEEVCENYKLA VNCFNNNRQCQCTSVGAQNTVICSKLAAKCLVM
MARGPGLAPPPLRLPLLLVLA AVTGHATAAQNCTCTPTNKMTVCSPDGGRCQCRALGSGMAVDCSTLTSTKCLLL
100
KAEMTHSKSGRR-MKP-EGAIQNNNDGLYDPECEQGLFKAKQCNGTATCWCVNTAGVRRTDK-DTEITC SERVRTY
KAEMTHSKSGRR- IKP-EG- IQNNNDGLYDPCDEQGLFKAKQCNGTATCWCVNTAGVRRTDK-DTEITC SERVRTY
KAEMNGSKLGR- AKP-EGALQNNNDGLYDPCDESGGLFKAKQCNGTSTCWCVNTAGVRRTDK-DTEITC SERVRTY
KARMSAPKNARTLVRPSEHALVDNDGLYDPCDPEGRFKAQCNQTSVCWCVNSVGVRRTDKGDLRLRCDLVRTH
200
WIIELKHKERAQPYNFESLHTALQDTFASRYMLNPKFIKSI MYENNVTITIDLMQNSSQKTQDDVDIADVAYYFEK
WIIELKHKERESPYDHQSLQALQEAFTSRYKLNQKFIKNI MYENNVTITIDLMQNSSQKTQDDVDIADVAYYFEK
WIIELKHKAREKPYDSKSLRTALQKEITTRYQLDPKFITSILYENNVTITIDLVQNSSQKTQNDVDIADVAYYFEK
HILIDLHRPTAGAFNHSDLD AELRLFRERYRLHPKFVAAVHYEQPTIQIELRQNTSQKAAAGEVDIGDAAYYFER
300
DVKGESLFHSSKSMDLRVNGELLDLDPGQTLIYYVDEKAPEFSMQGLTAGIIAIVVVVVLAVIAGIVVLVISTRKR
DVKGESLFHSSKSMDLRVNGEPLDLDPGQTLIYYVDEKAPEFSMQGLTAGIIAIVVVVSLAVIAGIVVLVISTRKK
DVKGESLFH-SKKMDLTVNGEQQLDLDPGQTLIYYVDEKAPEFSMQGLKAGVIAIVVVVMAVVAGIVVLVISTRKKR
DIKGESLFQGRGGLDLRVRGEPQLVE--RTLIIYYLDEI PPKFSSMKRLTAGLIAIVVVVVVALVAGMAVLVITNRRK
325
SAKYEKAEIKEMGEIHRELNA
SAKYEKAEIKEMGEIHRELNA
MAKYEKAEIKEMGEMHRELNA
SGKYKKVEIKELGELRKEPSL

Figure 6C

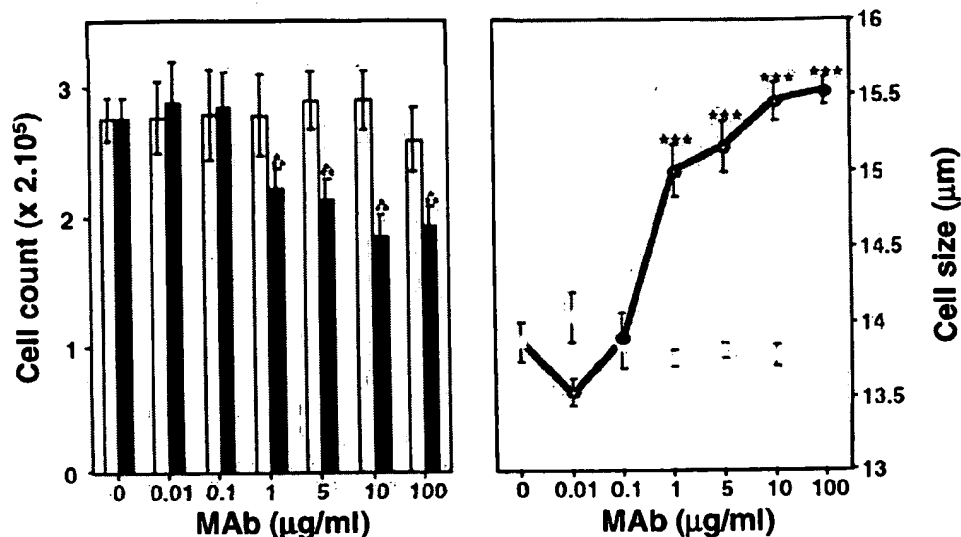


Figure 6 D

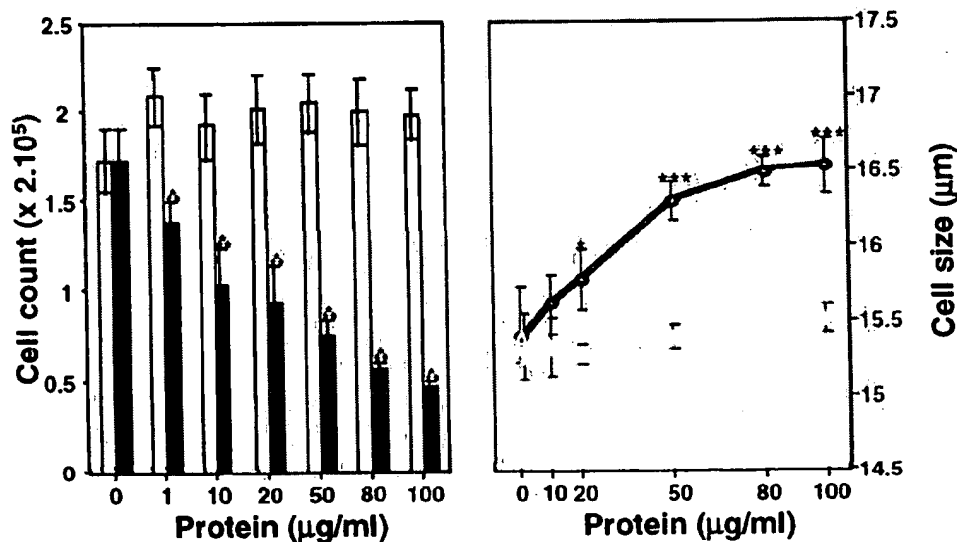
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A



B



C

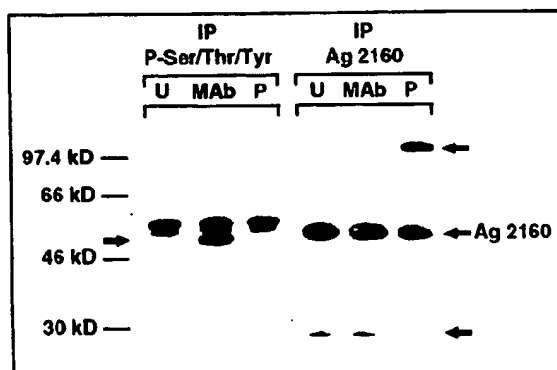


Figure 7

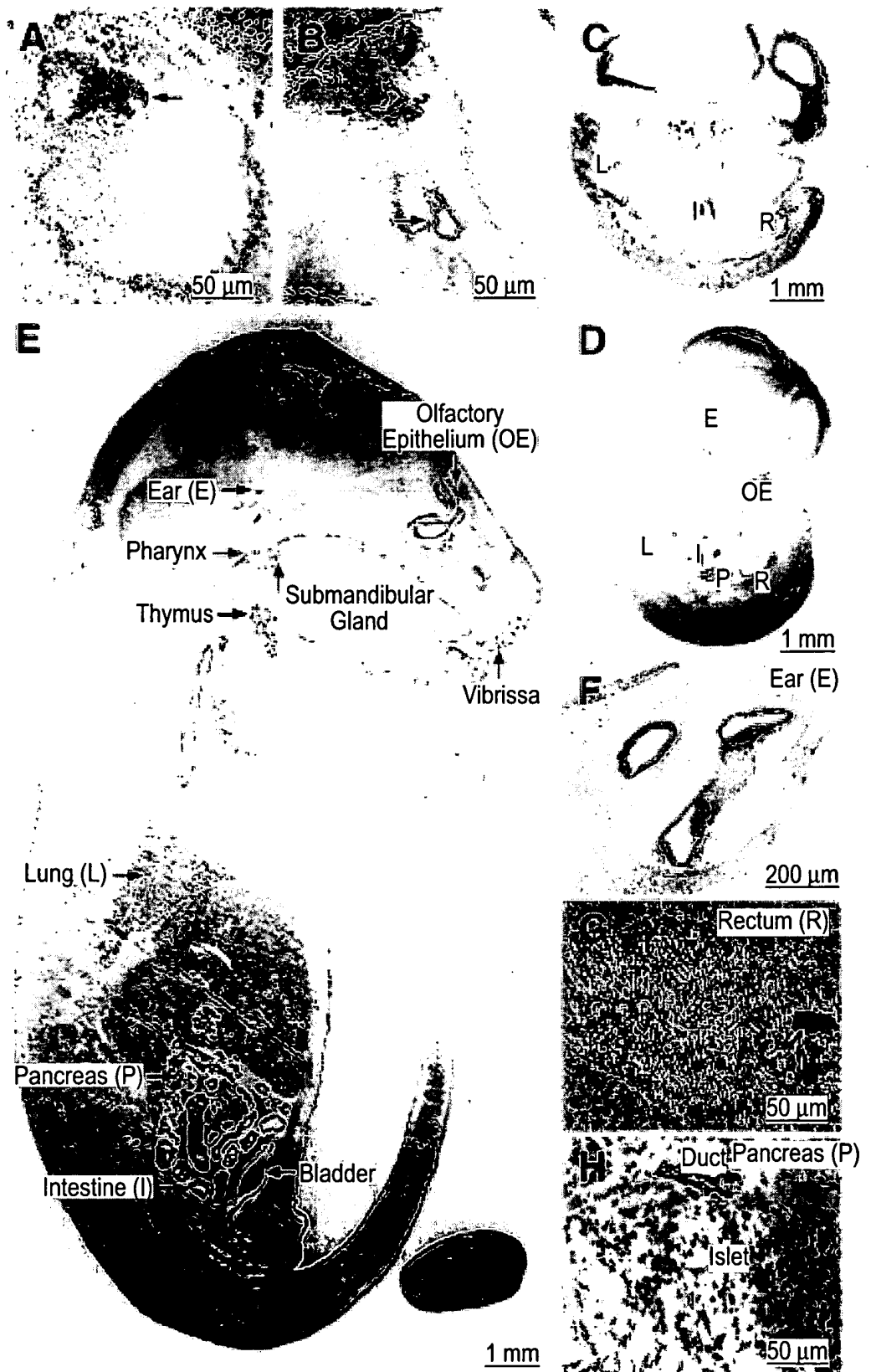


FIG. 8

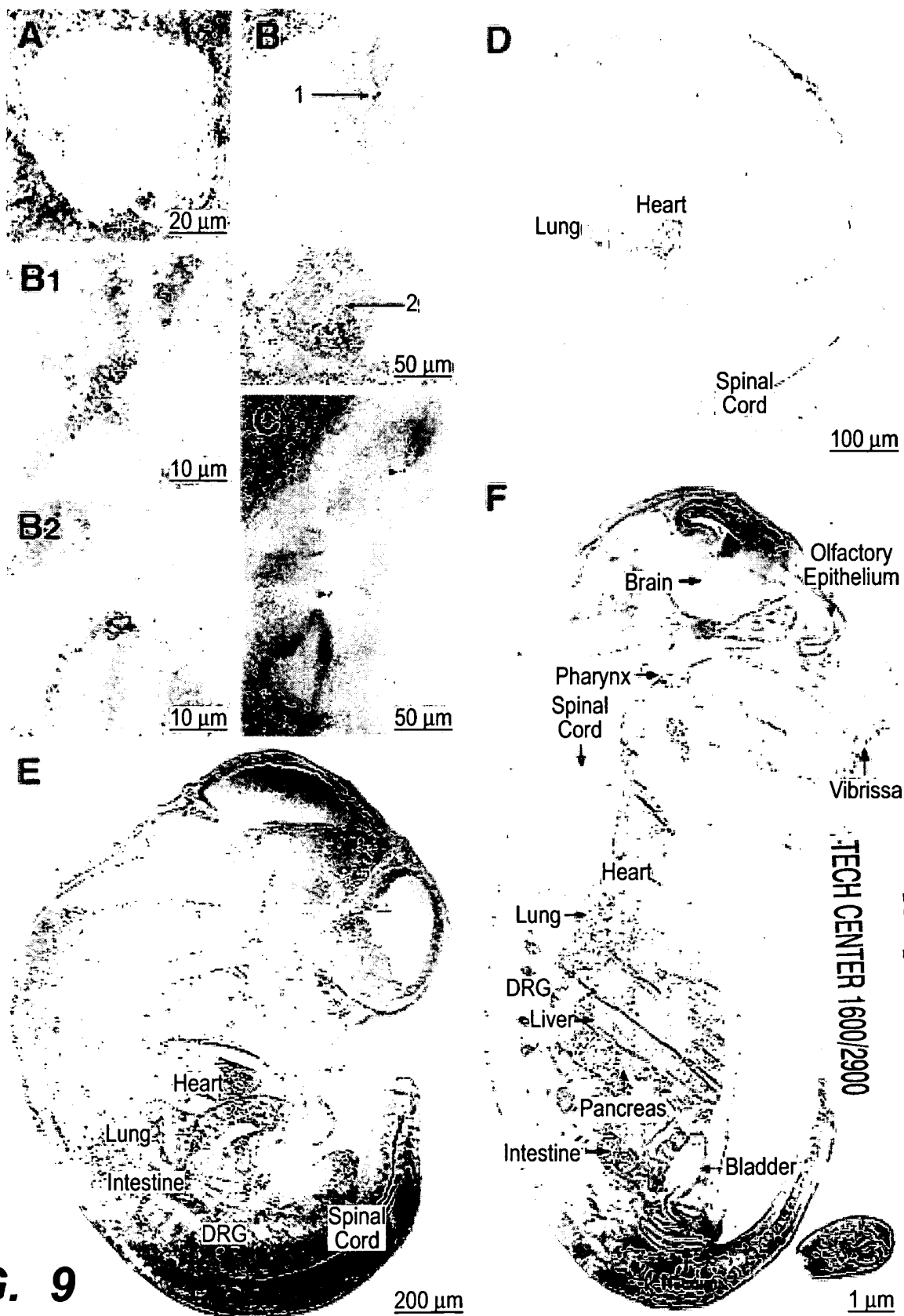
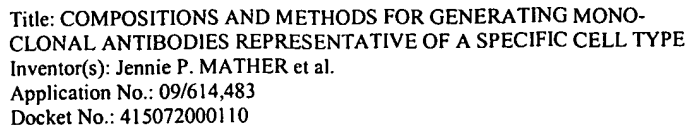


FIG. 9

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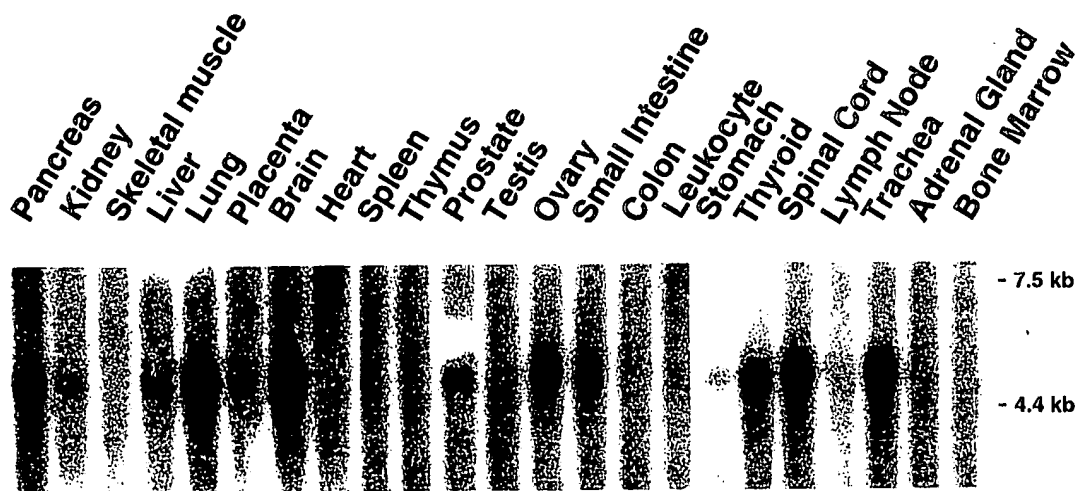
CACCTCGGTTCTATCGATTTCGAATTCGGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCTTGCTCTTCTTATCCTCTCTCTTCAAGAAGAGAAACTCTCGGAGACAGCAGCCAAA
AAAGAAACCGGCTCTACTTGACAGACTACTGAAGCGTCTCTGGAAATAAGAGGTCGCCCGCTTGGGAGTAGCAGCCAA
AGACCGCTGAGGGAGGGGTGTGGAGGGGGAGGAGGAGTTGCGGGTTCCGCGTGGAGGAAAGTTGCGTGTGGCACAGACCC
GACGGCGCAGCGCCACAGCGCCCGGGGATCGTGTCTTGAAAAAAAAGTCGCTGTCCCCCTAAAGCGAGACCCACAA
GCGAGCGGGCCCCGTGGGCCCGGGGACGACGCCCTCTCGCGCGTGGACTTTGTTCGGTGGCTTCTAGGAGGAGGAAT

1	ATGGCATCTAAAGGGTCCCTTCTTGCCGTCCTGTTTTCTGCGCTCTTGATCTCCGCCGGTCTCTCAGAACCAAGGCCTCGG	27
81	M--A--S--K--G--S--P--S--C--R--L--V--F--C--L--L--I--S--A--A--V--L--R--P--G--L--G--	
	ATGGTACACTGTCAACTCAGCATACGGAGATACCATTTGTTCATGCCTTGCAGACTGGATGTACCTCAGAACCTCATGTTTG	
	-W--Y--T--V--N--S--A--Y--G--D--T--I--V--M--P--C--R--L--D--V--P--Q--N--L--M--F--G	54
1161	GCAAATGGAATAATGAAAAGCCTGATGGTGCCCGATATTATTGCATTCAGATCTTCTACAAAAGAAAAGTGTGCAGTAT	
	--K--W--K--Y--E--K--P--D--G--S--P--V--F--I--A--F--R--S--S--T--K--K--S--V--Q--Y--	81
2241	GATGATGTACCAGAGTACAAGGACAGACTGAGCCTCTCAGAAAACCTACACTCTGTCTATCAACAATGCAAAAGATCAGTGA	
	D--D--V--P--E--Y--K--D--R--L--S--L--S--E--N--Y--T--L--S--I--N--N--A--K--I--S--D--	108
3321	CGAAAAGAGATTGTGTGCATGCTAGTGACCGAGGACAACGTGTTTGAGGCACCTACCCCTGGTCAAGGTGTTCAAGCAAC	
	-E--K--R--F--V--C--M--L--V--T--E--D--N--V--F--E--A--P--T--L--V--K--V--F--K--Q--P	135
4401	CATCTAAACCTGAAATTGTAAACAGAGCAGCGTTTCTTGAAAACAGAGCAGCTAAAAAAGTTAGGTGACTGCATTTCAAGA	
	--S--K--P--E--I--V--N--R--A--A--F--L--E--T--E--Q--L--K--K--L--G--D--C--I--S--R--	162
4481	GACAGTTACCCAGACGGCAACATCACGTGGTATAGGAATGGGAAAGTGCTACAGCCTGTTGATGGAGAGGTGTCCATACT	
	D--S--Y--P--D--G--N--I--T--W--Y--R--N--G--K--V--L--Q--P--V--D--G--E--V--S--I--L--	189
5561	TTTTAAAAAGGAAATTGATCCAGGTACTCAGTTGTATACCATGACTTCTCCTTGAGTACAAGACAACCAAGTCTGACA	
	-F--K--K--E--I--D--P--G--T--Q--L--Y--T--M--T--S--S--L--E--Y--K--T--T--K--S--D--I	216
6641	TACAAAATGCCATTCACTTGTGTGACATATTATGGACCTTCGGGCCAGAAAACAATTTATTCTGAACAAGCAATCTTT	
	--Q--M--P--F--T--C--S--V--T--Y--Y--G--P--S--G--Q--K--T--I--Y--S--E--Q--A--I--F--	243
7721	GATATTACTATCTACAGAGCAGGTGACAATACAAGTACTGCCACCACAAAAAATGCCATCAAAAGAGGGACAACATCAC	
	D--I--Y--Y--P--T--E--Q--V--T--I--Q--V--L--P--P--K--N--A--I--K--E--G--D--N--I--T--	270
882	CCTTCAGTGTGGGAAATGGCAACCCACCTCCTGAGGAGTTTCATGTTTACTTACCAGGGCAGGCTGAAGGCATAAGAA	

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FIGURE 11



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